We claim:

1. Streptococcus undecaprenyl pyrophosphate synthase in crystalline form.

2. A composition comprising the synthase of claim 1.

3. The synthase of claim 1 wherein the synthase comprises an amino acid sequence at least about 80% homologous to SEQ ID NO:1.

4. The synthase of claim 3 wherein the synthase is at least about 90% homologous to SEQ ID NO:1.

5. The synthase of claim 1 wherein the synthase comprises a first ligand binding site, a second ligand binding site, or both.

6. The synthase of claim 3 wherein the synthase comprises a first ligand binding site, a second ligand binding site, or both.

7. The synthase of claim 4 wherein the synthase comprises a first ligand binding site, a second ligand binding site, or both.

8. The synthase of any one of claims 5, 6, or 7, comprising at least one ligand.

9. The synthase of claim 8 wherein synthase is co-crystallized with said ligand.

10. The synthase of claim 8 wherein the ligand is selected from the group consisting of farnesyl pyrophosphate, (S)-farnesyl thiopyrophosphate, isoprenyl pyrophosphate, magnesium ion, and sulfate ion.

11. The synthase of any one of claims 5, 6, or 7, wherein the first ligand binding site is defined by at least one amino acid residue selected from the group consisting of Asp^{28}, Gly^{29}, Gly^{31}, Arg^{32}, Arg^{41}, Ala^{71}, Arg^{79}, Leu^{90}, Pro^{91}, and Phe^{143}.

12. The synthase of claim 5 wherein the first ligand binding site comprises at least about 80% of the amino acid residues selected from the group consisting of Asp^{28}, Gly^{29}, Gly^{31}, Arg^{32}, Arg^{41}, Ala^{71}, Arg^{79}, Leu^{90}, Pro^{91}, and Phe^{143}.

13. The synthase of claim 5 wherein the first ligand binding site comprises at least about 90% of the amino acid residues selected from the group consisting of Asp^{28}, Gly^{29}, Gly^{31}, Arg^{32}, Arg^{41}, Ala^{71}, Arg^{79}, Leu^{90}, Pro^{91}, and Phe^{143}.

14. The synthase of any one of claims 5, 6, or 7, wherein the second ligand binding site is defined by at least one amino acid residue selected from the group consisting of Asp^{28}, Arg^{200}, Arg^{206}, Ser^{208}, Glu^{219}(B), and Gly^{251}(B).

15. The synthase of claim 5 wherein the second ligand binding site comprises at least about 80% of the amino acid residues selected from the group consisting of Asp^{28}, Arg^{200}, Arg^{206}, Ser^{208}, Glu^{219}(B), and Gly^{251}(B).

16. The synthase of claim 5 wherein the second ligand binding site comprises at least about 90% of the amino acid residues selected from the group consisting of Asp^{28}, Arg^{200}, Arg^{206}, Ser^{208}, Glu^{219}(B), and Gly^{251}(B).

17. The synthase of any one of claims 5, 6, or 7, wherein the first binding site comprises Asp^{28}, Gly^{29}, Gly^{31}, Arg^{32}, Arg^{41}, Ala^{71}, Arg^{79}, Leu^{90}, Pro^{91}, and Phe^{143}, the second binding site comprises Arg^{200}, Arg^{206}, Ser^{208}, Glu^{219}(B), and Gly^{251}(B), or both.

18. The synthase of any one of claims 5, 6, 7, 12, or 13, wherein the first ligand binding site is capable of associating with farnesyl pyrophosphate, (S)-farnesyl thiopyrophosphate, or both.

19. The synthase of any one of claims 5, 6, 7, 15, or 16, wherein the second ligand site is capable of associating with isoprenyl pyrophosphate, sulphate, or both.

20. The synthase of claim 1 wherein the synthase comprises a first ligand binding site defined by amino acid residues 28, 29, 31, 32, 41, 71, 79, 90, 91, 143 having atoms having atomic coordinates according to Fig. 2.

21. The synthase of claim 1 wherein the synthase comprises a second ligand binding site defined by amino acid residues 28, 200, 206, 208, 219(B), and 250(B) having atoms having atomic coordinates according to Fig. 2.

22. The synthase of claim 1 wherein the synthase comprises *S. pneumoniae* undecaprenyl pyrophosphate synthase.

23. A composition comprising Streptococcus undecaprenyl pyrophosphate synthase and a substrate or substrate analog in crystalline form.

24. The composition of claim 23 wherein the substrate or substrate analog is co-crystallized with the synthase.

25. The composition of claim 23 wherein the substrate is farnesyl pyrophosphate.

26. The composition of claim 23 wherein the substrate is isoprenyl pyrophosphate.

27. The composition of claim 23 wherein the substrate analog is (S)-farnesyl thiopyrophosphate.

28. A method for identifying a potential ligand for an undecaprenyl pyrophosphate synthase, comprising:

(a) using a three-dimensional structure of the synthase as defined by at least atomic coordinates of amino acid residues 28, 29, 31, 32, 41, 71, 79, 90, 91, and 143 according to Fig. 2;

(b) employing the three-dimensional structure to design or select the potential ligand;

(c) obtaining the potential ligand; and

(d) contacting the potential ligand with the undecaprenyl pyrophosphate synthase to determine binding of the potential ligand to the synthase.

29. The method of claim 28 further comprising:

(e) identifying chemical entities or fragments thereof capable of binding to the synthase; and

(f) assembling the identified chemical entities or fragments thereof into a single molecule to provide the structure of the potential ligand.

30. The method of claim 28 wherein the ligand is an inhibitor.

31. The method of claim 30 wherein the inhibitor is a competitive inhibitor.

32. The method of claim 30 wherein the inhibitor is a noncompetitive inhibitor.

33. The method of claim 28 wherein the ligand is designed de novo.

34. The method of claim 28 wherein the ligand is designed from a known inhibitor.

35. The method of claim 28 wherein said synthase includes a ligand bound thereto, and the atomic coordinates, or a portion thereof, of said ligand are used according to step (a).

36. The method of claim 28 wherein the three-dimensional structure is further defined by atomic coordinates of amino acid residues 200, 206, and 208 according to Fig. 2.

37. The method of claim 28 wherein the three-dimensional structure is further defined by atomic coordinates of amino acid residues 219(B) and 250(B) according to Fig. 2.

38. The method of claim 28 wherein the potential ligand is designed to form a hydrogen bond with at least one amino acid residue selected from the group consisting of Gly^{29}, Gly^{31}, Arg^{32}, Arg^{41}, and Arg^{79}.

39. The method of claim 28 wherein the potential ligand is designed to form a hydrogen bond with at least one amino acid residue selected from the group consisting of Arg^{200}, Arg^{206}, Ser^{208}, Glu^{219}(B), and Gly^{251}(B).

40. The method of claim 28 wherein the potential ligand is designed to form a hydrophobic bond with at least one amino acid residue selected from the group consisting of Ala^{71}, Leu^{90}, Pro^{91}, and Phe^{143}.

41. The method of claim 28 wherein (c) precedes (b).

42. A method for identifying a potential inhibitor of a mutant undecaprenyl pyrophosphate synthase, comprising:

(a) using a three-dimensional structure of undecaprenyl pyrophosphate synthase as defined by atomic coordinates of undecaprenyl pyrophosphate synthase according to Fig. 2;

(b) replacing one or more undecaprenyl pyrophosphate synthase amino acids selected from 28, 29, 31, 32, 41, 71, 79, 90, 91, 143, 200, 206, 208, 219, and 250 of SEQ ID NO:1 in the three-dimensional structure with a different naturally occurring amino acid, thereby forming a mutant undecaprenyl pyrophosphate synthase;

(c) employing the three-dimensional structure to design or select the potential inhibitor; and

(d) contacting the potential inhibitor with the mutant undecaprenyl pyrophosphate synthase or the undecaprenyl pyrophosphate synthase in the presence of a substrate to test the ability of the potential inhibitor to inhibit the undecaprenyl pyrophosphate synthase or the mutant undecaprenyl pyrophosphate synthase.

43. The method of claim 42 wherein the potential inhibitor is selected from a database.

44. The method of claim 42 wherein the potential inhibitor is designed de novo.

45. The method of claim 42 wherein the potential inhibitor is designed from a known inhibitor.

46. The method of claim 42 wherein step (c) comprises:

(i) identifying chemical entities or fragments thereof capable of associating with the mutant undecaprenyl pyrophosphate synthase; and

(ii) assembling the identified chemical entities or fragments thereof into a single molecule to provide the structure of the potential inhibitor.

47. The method according to any one of claims 42-46 wherein the potential inhibitor is a competitive inhibitor of mutant undecaprenyl pyrophosphate synthase.

48. The method according to any one of claims 42-46 wherein the potential inhibitor is a non-competitive or uncompetitive inhibitor of mutant undecaprenyl pyrophosphate synthase.

49. A method of identifying a ligand capable of binding to an undecaprenyl pyrophosphate synthase substrate binding site, comprising:

(a) introducing into a suitable computer program information defining the binding site comprising first atomic coordinates of amino acids capable of binding to a synthase substrate, wherein the program displays the three-dimensional structure of the binding site;

(b) creating a three dimensional model of a test compound in the computer program;

(c) docking the model of the test compound to the structure of the binding site;

(d) creating a second three dimensional model of the substrate or an inhibitor of the synthase and docking the second model thereto; and

(e) comparing the docking of the test compound and of the substrate or the inhibitor of the synthase to provide an output of the program.

50. The method of claim 49 further comprising introducing into the computer program second atomic coordinates of water molecules bound to the substrate.

51. The method of claim 49 further comprising introducing into the computer program third atomic coordinates of at least one synthase structural element selected from the group consisting of an alpha helix, a 3_{10} helix, a strand of beta sheet, and a coil.

52. The method of claim 51 wherein the 3_{10} helix comprises the sequence Asn-Trp-Thr.

53. The method of claim 49 further comprising:

(f) incorporating the test compound into a biological or biochemical synthase activity assay; and

(g) determining whether the test compound inhibits synthase activity in the assay.

54. A method for identifying a potential inhibitor for an undecaprenyl pyrophosphate synthase, comprising:

(a) using a three-dimensional structure of the synthase as defined by atomic coordinates of undecaprenyl pyrophosphate synthase according to Fig. 2;

(b) employing said three-dimensional structure to design or select the potential inhibitor; and

(c) contacting the potential inhibitor with the synthase in the presence of a substrate to determine the ability of the potential inhibitor to inhibit the synthase.

55. The method of claim 54 wherein the potential inhibitor is designed de novo.

56. The method of claim 54 wherein the potential inhibitor is designed from a known inhibitor.

57. The method of claim 54 wherein step (b) comprises:

(i) identifying chemical entities or fragments thereof capable of associating with the synthase; and

(ii) assembling the identified chemical entities of fragments into a single molecule to provide the structure of the potential inhibitor.

58. The method of claim 57 wherein the potential inhibitor is designed de novo.

59. The method of claim 57 wherein the potential inhibitor is designed from a known inhibitor.

60. The method according to any one of claims 54 or 57-59, wherein the potential inhibitor is a competitive inhibitor of undecaprenyl pyrophosphate synthase.

61. The method according to any one of claims 54 or 57-59, wherein said potential inhibitor is a non-competitive or uncompetitive inhibitor of undecaprenyl pyrophosphate synthase.

62. A method for drug design comprising using atomic coordinates of a *S. pneumoniae* undecaprenyl pyrophosphate synthase having at least one ligand binding site to computationally evaluate relative associations of chemical entities with the ligand binding site and produce an output.

63. The method of claim 62 wherein the chemical entity is an intermediate in a farnesyl pyrophosphate elongation reaction, or an analog thereof.

64. A method for solving a crystal form comprising using atomic coordinates of a *S. pneumoniae* undecaprenyl pyrophosphate synthase crystal or portions thereof, to solve a crystal form of a mutant, homolog or co-complex of the undecaprenyl pyrophosphate synthase by molecular replacement.

65. The method of claim 64 comprising using atomic coordinates of a ligand bound to the undecaprenyl pyrophosphate synthase.

66. A machine-readable data storage medium comprising a data storage material encoded with machine-readable data comprising atomic coordinates comprising amino acid residues 28, 29, 31, 32, 41, 71, 79, 90, 91, and 143 according to Fig. 2.

67. The machine-readable data storage medium of claim 66 wherein the machine-readable data comprise atomic coordinates comprising at least one amino acid residue selected from the group consisting of 200, 206, 208, 219(B), and 250(B) according to Fig. 2.

68. The machine-readable data storage medium of claim 66 wherein the machine-readable data comprise the three-dimensional structure of *S. pneumoniae* undecaprenyl pyrophosphate synthase.

69. A computer-implemented tool for design of a drug, comprising:

(a) a three-dimensional structure of an undecaprenyl pyrophosphate synthase as defined by atomic coordinates of a *S. pneumoniae* undecaprenyl pyrophosphate synthase having at least one ligand binding site;

(b) a model of a chemical entity; and

(c) a computer program addressing the coordinates and capable of modeling the chemical entity in the ligand binding site to produce an output.

70. The tool of claim 69, wherein said atomic coordinates are essentially as described in Fig. 2.

71. A computer for producing a three-dimensional representation of an undecaprenyl pyrophosphate synthase ligand binding site comprising:

(a) a machine-readable data storage medium comprising a data storage material encoded with machine-readable data comprising the atomic coordinates comprising the amino acid residues 28, 29, 31, 32, 41, 71, 79, 90, 91, and 143 according to Fig. 2;

(b) a working memory for storing instructions for processing the machine-readable data;

(c) a central-processing unit coupled to the working memory and to the machine-readable data storage medium for processing the machine readable data into the three-dimensional representation; and

(d) a display coupled to the central-processing unit for displaying the three-dimensional representation.

72. The computer of claim 71 wherein the computer produces a three-dimensional representation of the ligand binding site of an undecaprenyl pyrophosphate synthase; and wherein the machine-readable data comprises the atomic coordinates of the ligand binding site.

73. A method of preparing Streptococcus undecaprenyl pyrophosphate synthase in crystalline form comprising incubating the synthase in a hanging drop.